Amendments to the Drawings:

Replacement Sheets of Figures 5 and 6 are attached hereto. Also attached is a marked-up copy of the drawings.

Figures 5 and 6 have been amended to show the sequence ID numbers for all illustrated sequences.

REMARKS/ARGUMENTS

Claims 1 - 16 are pending in the application.

Replacement Sheets of Figures 5 and 6 are attached hereto. Also attached is a marked-up copy of the drawings.

Figures 5 and 6 have been amended to show the sequence ID numbers for all illustrated sequences.

Amendments have been made to the specification to attend to the priority and sequence listing matters.

The rejection of claims 1-16 under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to use the invention, is respectfully traversed.

Claims 1-16 read as follows:

1. A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are symmetrically related and compete to effect gene expression regulation and outputting the result thereof to a user.

2. A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are symmetrically related and
cooperate to effect gene expression regulation and outputting the result thereof to a user.

3. A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are asymmetrically related and compete to effect gene expression regulation and outputting the result thereof to a user.

4. A method of identifying gene expression regulation mechanisms in a genome comprising detecting, by computer, the connectron pairs that are asymmetrically related and cooperate to effect gene expression regulation and outputting the result thereof to a user.

5. A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are symmetrically related and compete to effect gene expression regulation and outputting the result thereof to a user.

6. A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are symmetrically related and cooperate to effect gene expression regulation and outputting the result thereof to a user.

7. A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are asymmetrically related and compete to effect gene expression regulation and outputting the result thereof to a user.

8. A method of designing gene expression regulation mechanisms in a genome comprising modeling, by computer, the connectron pairs that are asymmetrically related and cooperate to effect gene expression regulation and outputting the result thereof to a user.

9. A method of genome investigation, by computer comprising identifying a new class of connectrons that bind to the major groove of double-stranded DNA in two directions and outputting the result thereof to a user.

10. A method of genome investigation, by computer, comprising designing one or more new classes of connectrons that bind to the major groove of double-stranded DNA in two directions and outputting the result thereof to a user.

11. A method of genome investigation, by computer, comprising identifying the relationship between an existing pair of connectrons in a genome and outputting the result thereof to a user.

12. A method of genome investigation, by computer, comprising designing the relationship between a synthetic pair of connectrons in a genome and outputting the result thereof to a user.

13. A computer mediated method for identifying the relationship between an existing pair of connectrons in a genome that act in a competitive mode such that with respect to the individual connectrons there is an increased lifetime of connectron control of a set of genes and outputting the result thereof to a user.

14. a computer mediated method for designing a synthetic pair of connectrons in a genome that act in a competitive mode such that with respect to the individual connectrons there is an increased

lifetime of connectron control of a set of genes and outputting the result thereof to a user.

15. A computer mediated method for identifying the relationship between an existing pair of connectrons in a genome that act in a cooperative mode such that with respect to the individual connectrons there is an increased lifetime of connectron control of a set of genes and outputting the result thereof to a user.

16. A computer mediated method for designing a synthetic pair of connectrons in a genome that act in a cooperative mode such that with respect to the individual connectrons there is an increased lifetime of connectron control of a set of genes and outputting the result thereof to a user.

In rejecting claims 1-16 under 35 U.S.C. 112, the Examiner contends at page 6 in section "a) Quantity of experimentation" the following:

> In order to practice the claimed invention one of skill in the art must identify and use a connectron to predict regulation of gene expression. In some embodiments changes in connectron behavior that correlate with changes in gene expression is monitored or effected...."

Further, the Examiner contends in paragraph b) on page 6 that:

> The specification does not provide guidance that there are any limitations on formation of triplex structures, and only implies that regions of RNA with identical sequence to one strand of a double stranded DNA sequence will form triplex structures. The specification does not address why all RNA transcripts of genes would not form a continuous triplex structure with the gene from which it is transcribed. The specification provides guidance to identify connectron symmetries in genomic sequences on pages 16-17. The specification does not provide detailed guidance to use identified connectron symmetries because the specification does not show whether or not connectrons form within cells or have an effect on gene expression. The specification does not provide specific guidance for monitoring or effecting changes in connectron behavior that correlate with gene expression.

In paragraph c) on page 5, the Examiner contends:

> However, the specification does not provide evidence that connectron symmetries in genomic sequences result in formation of triplex RNA-DNA structures or that if connectron triplex structures do exist that connectrons control gene expression. The specification does not provide working examples of using identified connectron symmetries to predict effects on gene expression. The specification does not provide working examples of monitoring or effecting changes in connectron behavior that correlate with gene expression.

Finally, in paragraph e) entitled "The state of the prior art" (paragraph bridging pages 7 and 8), the Examiner contends that:

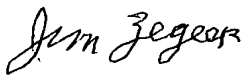
> One of skill in the art, after reading the specification, would not know that connectron symmetries identified by computer-mediated searches of genomic sequences would allow for prediction of gene expression of genes that have connectron symmetries. The specification does not provide experimental evidence that connectron symmetries cause modulation of gene expression.

In parent application Serial No. 09/866,925, the Board of Patent Appeals and Interferences issued a "Vacatur and Remand to the Examiner" dated September 28, 2006, a copy of which is attached. In that action, the Board analyzed claims 20 and 21 and vacated the Examiner's rejection contending that the Examiner "focuses on" an "issue" not claimed and pointed out that claim 20, for example, "does not require predicting regulation of gene expression, but only appears to require locating possible connectrons." Applicant respectfully submits that the same reasoning applies to the Examiner's rejection of claims 1-16 of the present application in that these claims as recited above do not require the features cited by the Examiner and quoted above. Hence, it is respectfully submitted that the Examiner has exceeded

the bounds of 35 U.S.C. 112, first paragraph, in rejecting the claims.

Further and favorable reconsideration is respectfully requested.

Respectfully submitted,



Jim Zegeer, Reg. No. 18,957
Attorney for Applicant

Attachments:
1. Computer Readable Disc of the Sequence Listing (3 copies)
2. "Vacatur and Remand to the Examiner" (issued in Ser. No. 09/866,925)
3. Replacements Sheets of Figures 5 and 6 (2 sheets)
4. Marked-Up Versions of Figures 5 and 6 (2 sheets)

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Date: August 28, 2007

In the event this paper is deemed not timely filed, the applicant hereby petitions for an appropriate extension of time. The fee for this extension may be charged to Deposit Account No. 26-0090 along with any other additional fees which may be required with respect to this paper.

UNITED STATES PATENT AND TRADEMARK OFFICE

BEFORE THE BOARD OF PATENT APPEALS AND INTERFERENCES

Ex parte RICHARD J. FELDMANN

Appeal No. 2006-2194
Application No. 09/866,925

ON BRIEF

Before ADAMS, GREEN, and LEBOVITZ, Administrative Patent Judges.

GREEN, Administrative Patent Judge.

VACATUR AND REMAND TO THE EXAMINER

On consideration of the record, we find that this case is not susceptible to meaningful review and is thus not in condition for a decision on appeal. Accordingly, we vacate the pending rejections and remand the application to the examiner to consider the issues discussed herein and take appropriate action not inconsistent with the views expressed herein. Lest there be any misunderstanding, the term "vacate" in this context means to set aside or void. When the Board vacates an examiner's rejection, the rejection is set aside and

no longer exists. Cf. Ex parte Zambrano, 58 USPQ2d 1312, 1313 (Bd. Pat. App. & Int. 2001).

BACKGROUND

According to the specification:

> This patent application shows how two specific adjacent RNA single-stranded sequences (called C1 and C2 – for Control Sequence 1 and Control Sequence 2) interact with two distant double-stranded DNA sequences (called T1 and T2 – for Target Sequence 1 and Target Sequence 2) to form a tetradic relationship which is called a "connectron." The two distant DNA double-stranded sequences (T1 and T2) must be on the same chromosome in a genome and they must be between 1kb and 105kb of each other. The adjacent single-stranded RNA sequences (C1/C2) can be on the same or different chromosomes as the T1 and T2 sequences. The C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence. The connectron acts to stabilize the double-stranded DNA by allowing 30nm chromatin particles to form. Genes that lie between T1 and T2 sequences when wrapped up in 30 nm chromatin particles are not open to promotion and expression.

Id. at 1-2.

Moreover,

> [c]haracteristically the adjacent C1/C2 sequences lie in the 3'UTR of a gene. The T1 and T2 sequences do not lie within the translated region of any gene. These sequences "surround" one or more genes.

Id. at 2.

A "possible connectron" is defined by the specification as:

> Any set of T1, T2 and C1/C2 sequences such that the C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence. The promoter of some gene causes the mRNA of the gene to be expressed. The mRNA is edited to eliminate the introns. The whole mRNA including the 3'UTR can move about in the cell or the nucleus of the cell. The C1/C2 RNA that is part of the 3'UTR moves to the T1 and T2 DNA sequences.

> A triple-stranded complex of the DNA and RNA forms such that the C1 sequence forms hydrogen bonds with the T1 sequence and the C2 sequence forms hydrogen bonds with the T2 sequence. Because the C1 sequence is adjacent to the C2 sequence, the T1 sequence is brought physically close to the T2 sequence. This produces a loop of between 1kb and 150kb in the DNA. Histone proteins reduce the length of the DNA by binding 200 bases. Histone/DNA complexes form six-fold symmetry chromatin assemblies. The diameter of the chromatin assemblies is approximately 30nm.

Id. at 6-7.

The specification states that an algorithm has been developed "to determine the connectron structure of any genome," Id. at 2, and Figure 8 provides an overall view of the algorithm, see id. at 25. The "connectron invention" "depends only on sequence equivalency." Id. at 28. As can be seen in Figure 8, the algorithm analyzes a genome for possible connectrons. Moreover, according to the specification, the physical experimentation process of proving the existence and lifetimes of connectrons "is logically quite separate from the computational experimentation that have been conducted from June of 1999 to May of 2001," id. at 28, which has demonstrated the existence of connectrons in prokaryotes, plants, higher animals and humans using publicly available genomes, see id. at 35, 37 and 38.

Claim 20, which is only one of the eight independent claims, is drawn to:

> A computer mediated method of identifying DNA sequences that control the expression of different collections of genes in a genome comprising detecting, by computer, one or more pairs of first and second non-adjacent DNA sequences which could bind to one RNA molecule such that a first RNA sequence in that RNA molecule can bind a first non-adjacent DNA sequence and a second RNA sequence in that RNA molecule can bind to a second non-adjacent sequence.

VACATUR AND REMAND

The board serves as a board of review, not a de novo examination tribunal. See 35 U.S.C. § 6(b) ("The [board] shall, on written appeal of an applicant, review adverse decisions of examiners upon applications for patents."). The burden is on the examiner to set forth a prima facie case of nonpatentability. See In re Alton, 76 F.3d 1168, 1175, 37 USPQ2d 1578, 1581 (Fed. Cir. 1996).

Claims 20-37, all of the claims on appeal, stand rejected under 35 U.S.C. § 112, first paragraph, as containing subject matter that was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The rejection is set forth on pages 3-5 of the Examiner's Answer, but it suffers from several deficiencies.

First, there are eight independent claims, each having different limitations. For example, claim 21 requires "detecting, by computer, changes in connectron behavior in the genome as a function of changes in the sequence of the genome." The rejection, however, does not address the limitations of all of the independent claims, nor does it address the limitations of dependent claims 37.

Second, the rejection appears to address limitations that do not seem to appear in the claims. The examiner focuses on the issue that "[i]n order to practice the claimed invention one of skill in the art must identify and use a connectron to predict regulation of gene expression." Examiner's Answer, page

3. Claim 20, for example, does not require predicting regulation of gene expression, but only appears to require locating possible connectrons.

Last, and most importantly, neither the examiner nor appellant appears to have engaged in any sort of claim construction, nor have they appeared to have reached a "meeting of the minds" on how the claims should be interpreted. As set forth in In re Zletz, 893 F.2d 319, 321-22, 13 USPQ2d 1320, 1322 (Fed. Cir. 1989):

> [D]uring patent prosecution when claims can be amended, ambiguities should be recognized, scope and breadth of language explored, and clarification imposed. . . . An essential purpose of patent examination is to fashion claims that are precise, clear, correct, and unambiguous. Only in this way can uncertainties of claim scope be removed, as much as possible, during the administrative process.

Moreover, we remind the examiner and appellant that analyzing claims based on "speculation as to meaning of the terms employed and assumptions as to the scope of such claims" is legal error. In re Steele, 305 F.2d 859, 862, 134 USPQ 292, 295 (CCPA 1962).

Thus, upon return of the application, the examiner should engage in the claim construction analysis, and address any issues that may arise based on that analysis. For the convenience of the examiner and appellant, we have provided some examples of such issues, but this should not be seen as an exhaustive of all such issues that may exist.

Claim 20 appears to be drawn to a method of detecting pairs of non-adjacent DNA sequences which can bind to two regions of an RNA molecule. As such, the claim is very broad, and is not limited to identifying "connectrons."

Francois[1] teaches that "oligonucleotides consisting of two oligimer sequences linked by a chemical tether can also bind two single-stranded noncontiguous sites in RNA with secondary structures." Id. at page 65, column 2. Thus, it would have been obvious to thus use a computer design the oligonucleotide consisting of two oligomer sequences (reads on a pair of non-adjacent DNA sequences" and then predict its binding to the noncontiguous sites of the RNA (reads on two regions of an RNA molecule), which appears to be all that is required by claim 20.

Claim 22 recites "detecting [by computer] changes in expression of different gene collections in a genome that result in the level of control sequences caused by exogenous stimuli." At first blush, this claim appears to have many issues.

One issue appears to be that the claim is indefinite under 35 U.S.C. § 112, second paragraph. It is unclear if the exogenous stimuli is physical or computational. If it is physical, it is unclear how that step is being performed in the context of the computational method.

If the exogenous stimuli is computational, the claim would not appear to meet the written description and/or enablement requirements of 35 U.S.C. § 112, first paragraph.[2] As discussed in the background, the specification teaches a

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[1] Francois et al. (Francois), Recognition and Cleavage of Singgle-Stranded DNA Containing Hairpin Structures by Oligonucleotides Forming Both Watson-Crick and Hoogsteen Hydrogen Bonds," Biochemistry, Vol. 34, pp. 65-72 (1995), first page only.

[2] We recognize that the written description and enablement requirements of 35 U.S.C. § 112, first paragraph, are distinct, and should be analyzed separately. See Vas-Cath Inc. v. Mahurkar, 935 F.2d 1555, 1563-64, 19 USPQ2d 1111, 1116-17 (Fed. Cir. 1991) (noting that the requirement for written description under the first paragraph of section 112 is separate and distinct from the

computational method of identifying possible connectrons, which is entirely separate from the physical experimentation process. First, the specification does not appear to describe a process of computationally adding exogenous stimuli and then looking at the level of connectron control. Second, such a claim would not appear to be enabled as the specification does not teach an algorithm which could perform such a calculation, nor does it teach what type of stimuli may be applied, or the correlation between any such stimuli and connectron control.

We note that similar issues appear to exist for each of the remaining independent claims.

Claims 28-37 all depend from claim 20, and state "[u]sing the method as defined in claim 20." A "use" or "using" claim, however, is not statutory subject matter, and the claims should be rejected under 35 U.S.C. § 101. See MPEP 2173.05(q). In addition, the examiner may wish to also explore a rejection under 35 U.S.C. § 112, second paragraph, as it is unclear what method steps are being added by these dependent claims to the method set forth in claim 20.

Again, these examples are not exhaustive, and the examiner should undertake a more thorough analysis of all the claims as to whether they meet the statutory requirements of § 101, § 102, § 103 and § 112.

FUTURE PROCEEDINGS

The case is being returned to the jurisdiction of the examiner for further action not inconsistent with this opinion.

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enablement requirement of that paragraph). We only discuss them together here for the sake of expediency.

If prosecution is resumed, we state that we are not authorizing a Supplemental Examiner's Answer.

VACATED and REMANDED

Donald E. Adams)
Administrative Patent Judge)
)
) BOARD OF PATENT
Lora M. Green)
Administrative Patent Judge) APPEALS AND
)
) INTERFERENCES
Richard M. Lebovitz)
Administrative Patent Judge)

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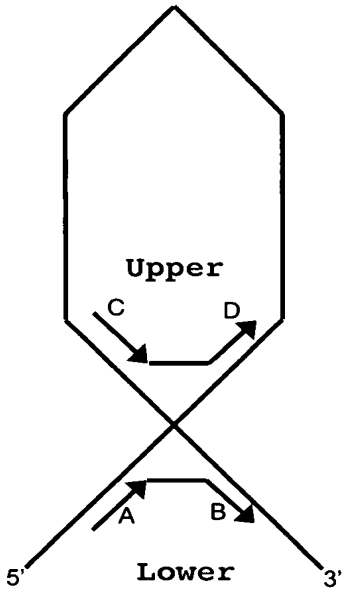
Marked-Up Version
S.N 10/803,195



(a) Concise representation of an Asymmetric Lower-Upper Connectron Pair

(b) Detailed Representation of an Asymmetric Lower-Upper Connectron Pair

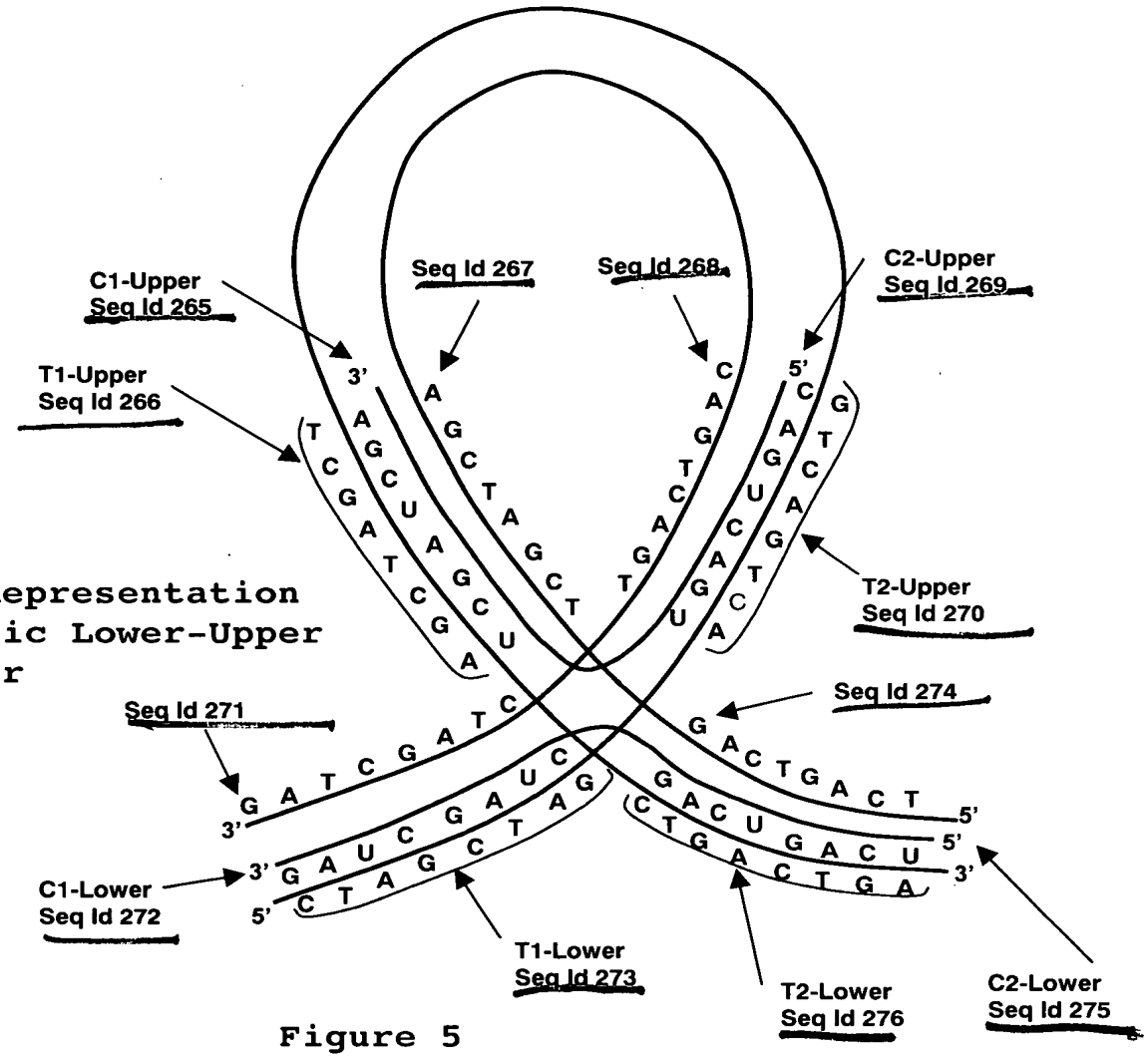
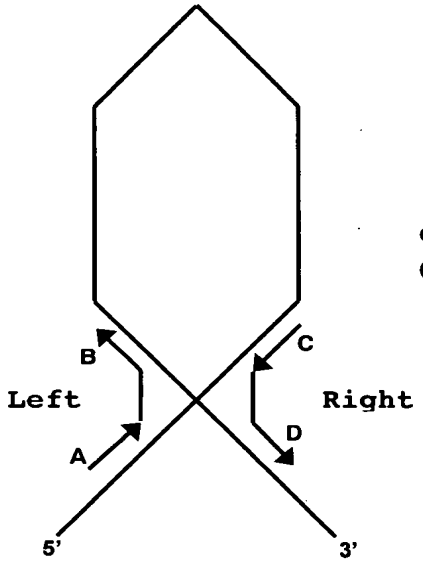


Figure 5

Marked-Up Version
S.N. 10/803,195



(a) Concise Representation of an Asymmetric Left-Right Connectron Pair.

(b) Detailed Representation of an Asymmetric Left-Right Connectron Pair

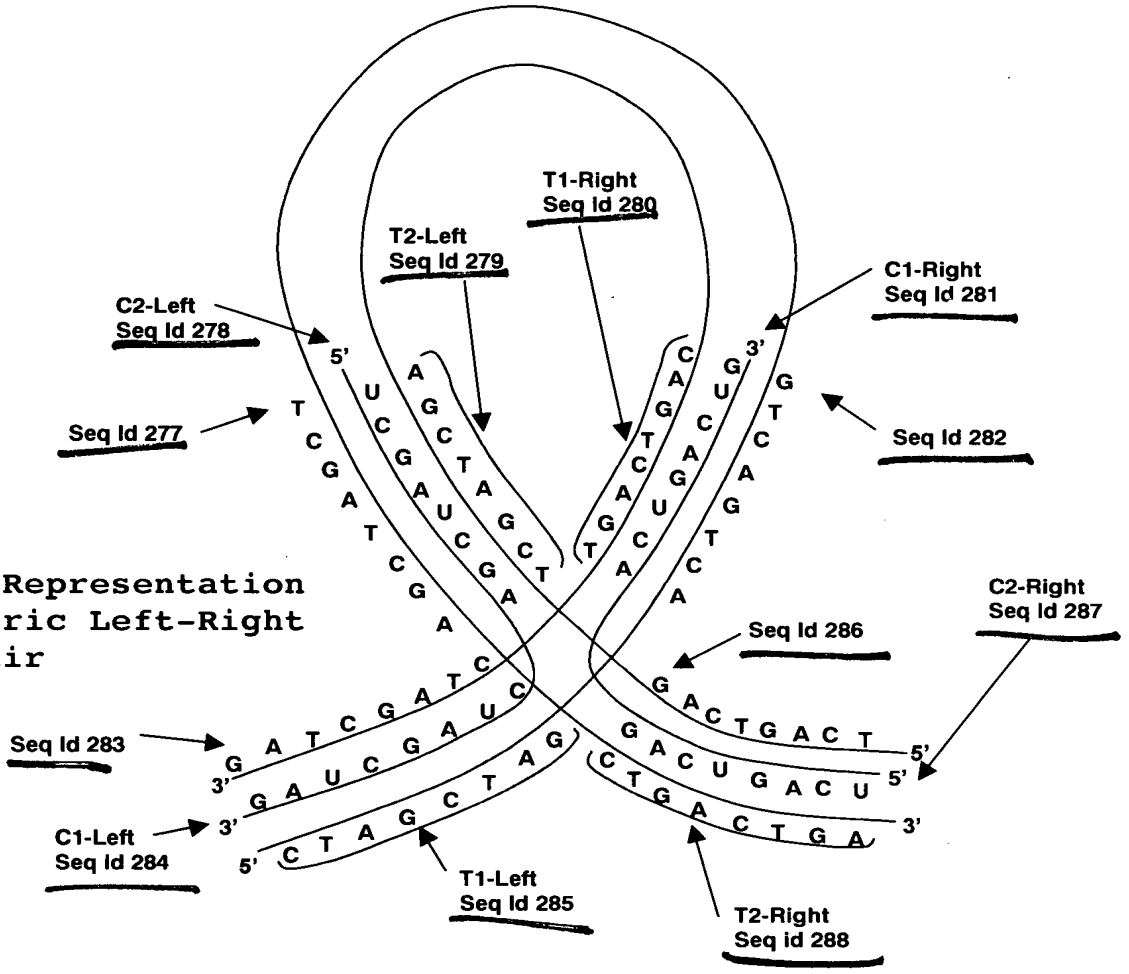


Figure 6